

REMARKS UNDER 37 CFR § 1.111

Formal Matters

Claims 1-75 are pending after entry of the amendments set forth herein.

Claims 1-75 were examined. Claims 1-75 were rejected.

Applicants respectfully request reconsideration of the application in view of the amendments and remarks made herein.

No new matter has been added.

The Office Action

Claims Provisionally Rejected Under 35 U.S.C. Section 101

In the Official Action of March 30, 2006, claims 32-36 were provisionally rejected under 35 U.S.C. Section 101 as claiming the same invention as that of claims 111-116 of co-pending Application No. 10/641,492. In view of the above amendment of claims 32-36, the Examiner is respectfully requested to reconsider and withdraw this provisional ground of rejection. Specifically, claims 111-116 of the co-pending application do not recite extracting nouns and verbs from at least a portion of a textual document, or a list based editor that lists nouns and verbs.

Claims Provisionally Rejected Under Nonstatutory Obviousness-Type Double Patenting

Claims 1-31, 38-66 and 68-75 were provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 111-116 of co-pending Application Serial No 10/641,492. The Examiner asserted that the subject matter claimed in the instant application is fully disclosed in the referenced co-pending application and would be covered by any patent granted on that co-pending application since the reference co-pending application and the instant application are claiming common subject matter and because the claims 111-116 of co-pending Application Serial No 10/641,492 contain every element recited in the rejected claims. Although Applicants do not necessarily agree with this provisional ground of rejection, particularly in view of the

above amendments, and thus do not acquiesce thereto, Applicants request that the Examiner hold this ground of provisional rejection in abeyance until such time as Application Serial No. 10/641,492 actually issues.

Claims Rejected Under 35 U.S.C. Section 112, Second Paragraph

Claims 1-37 and 58-60 were rejected under 35 U.S.C. Section 112, second paragraph as being indefinite. With regard to claims 1-37, the Examiner asserted that the use of the language “may be” in claims 1, 20, 24, 30 and 32 rendered these claims indefinite. In response thereto, Applicants have amended each of claims 1, 20, 24, 30 and 32 above to delete the phrase “may be” and replace it by a positive recitation in each case. Accordingly, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1-37 as being no longer appropriate.

As to claims 58-60, the Examiner asserted that there was no suggestion of a result being obtained in claim 38, and that therefore claims 58-60 were vague and indefinite. In response thereto, Applicants have amended claims 58-60 above to clarify that said result comprises at least one of a list created by said listing and a listed interaction having had directionality assigned thereto by said step of assigning directionality. In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 58-60 as being no longer appropriate.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1-37 and 58-60 rejected under 35 U.S.C. Section 112, second paragraph as being indefinite, as being no longer appropriate.

Claims Rejected Under 35 U.S.C. Section 102(e) (Hogue et al.)

Claims 1-75 were rejected under 35 U.S.C. Section 102(e) as being anticipated by Hogue et al., U.S. Patent No. 6,745,204. With regard to claim 1, The Examiner asserted that Hogue et al. discloses a tool providing interactive capabilities for user involvement in extracting and disambiguating biological information in text, wherein the tool includes a text viewer into which at least a portion of a textual documents may be imported and viewed. The Examiner further asserted that Hogue et al. discloses means for text mining the at least a portion of a textual document having been imported into the text viewer. The Examiner referenced column 7, lines 19-22 and lines 58-63 as support for the disclosure of means for text mining by Hogue et al.

Applicants respectfully traverse this position. It is respectfully submitted that column 7, lines 19-22 state that the invention of Hogue et al is BIND and its related tools for both the management and mining of molecular interaction data. No mention of text mining is made in the referenced lines. Likewise, column 7, lines 58-63 of Hogue et al. disclose that the design and database samples and tools to aid in web-based data entry and retrieval are described, and that a graphical system of data retrieval and data mining agents are provided that scour the data space for novel links between known interaction pathways. Again there is no mention of text mining.

Further, Hogue et al. goes on to describe that the BIND data model includes three main types of data objects: interaction, molecular complex and pathway. Each of the objects is composed of various descriptor objects that are either defined in the specification or taken from the NCBI ASN.1. For example, an interaction record contains two BIND objects. For example, a BIND object may describe a protein sequence, or store a simple link to a sequence database.

An optional free flow text description of the BIND object may be provided with the BIND object. However, this is simply a data field that is fillable with text to use as descriptor of the BIND object and is not related to text mining, see, for example, column 10, lines 55-58.

The BIND-Molecular-Complex object is meant to store a collection of more than two interactions that form a complex, i.e., three or more BIND objects that can operate as a unit, e.g., see column 15, lines 5-12.

The BIND-Pathway object describes a collection of more than two interactions that form a pathway, e.g., see column 16, lines 15-21.

An additional object, referred to as a BIND-pub-set is provided to hold all publications in BIND. A publication set contains a list of BIND-pub-objects and a dispute flag. A BIND-pub-object contains an optional free text description of the publication, an enumerated opinion of the publication field and a NCBI Pub object. The description field may hold any text data pertaining to the publication referenced by this object. This description field is also presumably manually filled out by a user, as there is no teaching or description of text mining to accomplish this task.

As noted at column 18, lines 49-50, BIND may rely upon different sources for data entry. Data may be entered manually using web based forms (column 18, lines 51-57), where BIND indexers review and validate the public entries as they arrive. Data that is already present in the literature will reportedly be entered into BIND, presumably manually, as this disclosure is under the Manual Data Entry heading. Automated data entry may also be carried out as described at column 18, line 4. Data gathering agents will gather protein multimers, protein-protein interactions and other interactions and compounds from

Structure, interaction and compound databases. There is no disclosure of accessing textual documents, data mining textual documents and extracting nouns and verbs from textual documents. Data may also be entered directly from experimental systems, but again this is interaction data, and the experiments are not described as textual documents.

The data mining that is disclosed by Hogue et al. at column 20, lines 9-13, refers to using a spider to traverse BIND to search for new signaling pathways. The spider searches the objects in BIND, traversing all pathway cross talk links looking for signaling routes that are not presently within BIND. This is not textual data mining, but rather an analysis of the interconnectivity of the information as it is linked in the BIND database.

BIND can be used to identify a biomolecular interaction that is similar to a reference biomolecular interaction stored in BIND. However, this describes a search for a network, or other graphical structure, and no description of text mining is disclosed or suggested. The test that is described is run on a test biomolecular interaction, where a similarity search is performed for each molecule.

In contrast, present claim 1 recites means for text mining at least a portion of a textual document. Hogue et al. neither discloses nor suggests text mining. To further clarify this distinction, claim 1 has been amended above to recite that the text mining extracts nouns and verbs from the at least a portion of a textual document. Support for this amendment can be found for example, at paragraphs [0046] and [0047] and throughout the specification. It is respectfully submitted that there is clearly no disclosure of extracting nouns and verbs from a textual document in Hogue et al.

With regard to claim 2, the Examiner asserted that Hogue et al. disclose means for representing the entities and interaction in a local format. Applicants respectfully disagree. Claim 2 depends from claim 1 and has been amended to clarify that the nouns and verbs that are extracted from the textual document are converted to the local format representation as the entities and interactions recited in claim 1. Hogue et al., column 7, lines 53-55 state that BIND draws upon NCBI data format standards, so that BIND is compatible with other public sequence and structure databases (emphasis added). This further reinforces the notion that Hogue et al. does not text mine or extract text from textual documents, as Hogue et al. is designed to be compatible with public sequence databases and structure databases. Further, since BIND is compatible with these bases, there is no conversion to a local format described. Hogue et al., column 7, lines 40-47 describe electronic management, location and/or visualization of interactions. BIND can store interaction information as a pointer to another database, a sequence, or a chemical graph. None of these possibilities refer to text or text having been converted to a local format.

As to claim 3, the Examiner asserted that Hogue et al. discloses the tool of claim 2, further comprising means for generating, displaying and interactively manipulating a biological diagram, based upon the entities and interactions represented in the local format. The Examiner referred to Figure 13 and column 3, lines 1-15 of Hogue et al. Fig. 13 is a schematic diagram showing the major components of the BIND system. Column 3, lines 1-15 describe that the BIND system includes: a maintenance entity for receiving data on biomolecular interactions from a plurality of providers and means for receiving and processing such data to create and maintain images and/or text defining biomolecular interactions. As noted above, Applicants again respectfully submit that the BIND system does not data mine textual documents or extract nouns and verbs from textual documents, as Hogue et al. specifically describe the system as being provided for interacting with other public sequence and structure databases, column 7, lines 40-47. The text defining biomolecular interactions that Hogue et al. refers to here is text that is inputted manually by a user into an optional free flow text description (e.g., see column 10, lines 5-12), and has nothing to do with data mining textual documents or extracting words from textual documents.

Column 3, lines 1-15 continue to describe that the BIND system may have one or more computer systems maintained by the maintenance entity and having means for creating and transmitting to a plurality of end users the images and/or text defining biomolecular interactions. Hogue et al. discloses that the system is useful in managing, finding and/or displaying biomolecular interactions including interactions involving proteins, nucleic acids (RNA, DNA), and ligands, molecular complexes, and signaling pathways. The interactions are defined both at the molecular and atomic levels and in particular they may be defined by chemical graphs. It is respectfully submitted that this portion of the Hogue et al. disclosure also fails to mention anything about text mining textual documents, extracting nouns and verbs from textual documents, or converting extracted text to a local format. BIND was developed to identify structural representations of interactions, such as chemical graphs, pathways, etc., and there is no disclosure or suggestion of extracting text from textual documents, or converting the extracted text to a local format.

With regard to claim 4, the Examiner asserted that Hogue et al. describes entities and interactions listed, where each listed entity and interaction points back to a location of the portion of the textual document where it was identified. The Examiner referred to column 8, lines 5-12 of Hogue et al. Column 8, lines 5-12 of Hogue et al. indicate that an interaction record contains two BIND-objects, and that these BIND-objects are themselves defined using simpler sub objects. Normally, a BIND-object that is describing a protein sequence will store a simple link to a sequence database, such as GenBank.

If the sequence is not present in the public database, it can be fully represented using an NCBI-Bioseq object. Neither of these techniques refer to an entity and interaction list, wherein each entity and interaction listed points back to a location of a portion of a textual document from where the verb or noun was extracted. The first technique points to a sequence database, which contains sequences, not textual documents. The second technique is a direct representation of a sequence, and does not point back to anything.

With regard to claim 5, the Examiner referred to column 3, lines 29-46 and column 7, lines 46-53 of Hogue et al., and asserted that Hogue et al. discloses means for assigning including slots associated with each said interaction, to which a user can identify one or more of said entities involved in the interaction, and assign roles of each said entity played in the interaction. Column 3, lines 29-46 of Hogue et al. disclose describe a “record” of BIND, which refers to a row in a database table. Each record contains one or more fields. A record of a biomolecular interaction may contain information identifying the interaction as a chemical graph and may contain a plurality of other attributes, such as the cellular place of interaction, experimental conditions used to observe the interaction, conserved sequence comment of molecules in the interaction if they are biological sequences, information on the molecules in the interaction, description of metabolic and signaling pathways, cell cycle stages in which an interaction is involved, location of binding sites on the molecules in an interaction, chemical action mediated by the interactions, and chemical states of the molecule in the interactions. Column 7, lines 46-53 disclose that two BIND-objects that interact are held in an interaction record within BIND. BIND can also store kinetic information, bibliographic information, interaction locations, conserved sequences, mediating interaction, chemical reactions that take place and activation states of BIND-objects. It is respectfully submitted that none of the disclosure referred to by the Examiner discloses or suggests means for text mining at least a portion of a textual document having been imported into a text viewer, extracting nouns and verbs from the at least a portion of the textual document having been imported, listing the extracted nouns and verbs as entities and interactions with a list-based text editor, or assigning directionality to the listed interactions, by user-assigned roles. It is further respectfully submitted that the referred to portions of Hogue et al. do not even disclose or suggest assigning roles that entities play in an interaction, and clearly do not disclose extracting nouns and verbs from text as claimed.

As to claim 6, the Examiner asserted that Hogue et al. discloses assignment of roles including affectors, affected and unassigned. The Examiner referred to Fig. 8, column 10, lines 26-33 and column 12, lines 40-47. Fig. 8 illustrates a BIND action object and associated components, and the brief description of Fig. 8 indicates that any number of chemical actions may be stored in an interaction.

Column 10, lines 26-33 describe a Bind-descr object and discloses that this object stores most of the information in an interaction object, that it contains text description of the interaction, information on cellular place of interaction, experimental conditions used to observe the interaction, conserved sequence comment of molecules A and/or B if they are biological sequences, location of binding sites on molecules A and B, chemical actions mediated by the interaction and chemical states of the molecules A and B. Column 12, lines 40-47 disclose a set of BIND-actions to describe the chemical action(s) mediated by an interaction, and refer to Fig. 8. A BIND-action set contains a set of elaborate BIND-action objects. Each BIND-action object in a set is numbered with an Internal-action-id (IAID) integer so that it can be referenced by other data types. None of the referred to disclosures mention assigning roles of “affected” affecters” or “unassigned” to entities that form an interaction. Further, it is respectfully submitted that the text description of the interaction is a free form textual description that is inputted by a user, and is not a role assignment, nor is it the result of extracting nouns and verbs from a textual document.

With regard to claim 7, the Examiner asserted that Hogue et al. discloses the assignment of roles comprising mediator and unknown by a user to entities involved in an interaction. Column 12, lines 51-67 of Hogue et al., which the Examiner referred to as support for this assertion, refers again to the IAID number, optional text description field for free flow text description of the chemical action, and an optional BIND-pub-set for storing publications pertaining to this chemical action. A Boolean flag is included to specify the direction of the chemical action. The type of action is identified in the BIND-action-type object. Types may include not specified, add, remove, cut-seq, change-conformation, change-configuration, change-other and other. Although Hogue et al. does disclose that a BIND-action-type object may store a “not-specified” type of chemical action, Hogue et al. does not disclose or suggest a user assigning roles to entities that have been listed as a result of extracting nouns from a textual document and listing them as entities in a text editor, wherein the user assigns a role relative to the entity’s part played in an interaction identified by a listed interaction.

As to claim 8, the Examiner asserted that Hogue et al. discloses the tool of claim 1 and further discloses a user context, wherein said means for text mining mines based upon contents of the user context. It is respectfully submitted that Hogue et al. does not disclose or suggest the tool of claim 1, for reasons provided above with regard to claim 1. The Examiner referred to column 2, lines 1-4 of Hogue et al. as support for disclosure of the claimed user context. Column 2, lines 1-4 disclose maintenance of a database of biological data that includes simple binary interaction to large-scale molecular complexes and network of pathways and interactions. The computer described can maintain the database, and

support the creation of advanced queries and querying tools and development of computer programs that use the information for data visualization, data mining, and visual data entry. It is respectfully submitted that the referred to lines of Hogue et al. do not disclose or suggest a user context as defined in the present specification. The user context provided entities and/or interactions that are used by the tool of claim 1 to facilitate identification and extraction of nouns and verbs from textual documents. Hogue et al. describes a database of molecular complexes and pathways, not textual documents.

With regard to claim 9, the Examiner asserted that Hogue et al. discloses at column 7, lines 58-63, a user context as claimed that comprises at least one entity or interaction. Column 7, lines 58-63 disclose tools to aid in web-based data entry and retrieval. A graphical system of data retrieval and data mining agents that scour this data space for novel links between known interaction pathways can be implemented based on this design (emphasis added). Again, Applicants respectfully submit that the disclosure of Hogue et al. is directed to a graphical system of data retrieval and data mining, and that data mining is for pathways and other graphical structures. No data mining of textual documents to extract nouns and verbs therefrom is disclosed or suggested by Hogue et al.

As to claim 10, the Examiner asserted that Hogue et al. discloses, at column 20, lines 10-19, means for managing user context that permits editing of an existing user context, as well as creation of a new user context. Applicants respectfully disagree. Column 20, lines 10-19 disclose a spider that traverses the BIND database searching for new signaling pathways. Thus, the spider traverses graphical structures, i.e., pathways, not textual documents. The new found pathways can then be experimentally evaluated. There is no disclosure here of a user context, or of editing a user context.

Regarding claim 11, the Examiner asserted that Hogue et al. further discloses means for managing that allows selection of specific entities and interactions to be added to a user context. The Examiner referred to column 5, lines 16-35 and 46-54 and column 6, lines 26-32. Column 6, lines 16-35 describe a computer system having a database with a plurality of records, each containing a reference biomolecular interaction defined by a chemical graph and descriptive information from an external database, a processor in communication with the database, and a user interface that allows a user to provide user input to the processor to selectively view information regarding a biomolecular interaction. It is respectfully submitted that this portion of Hogue et al. does not describe or suggest a user context as defined in the present specification, wherein the user context provides entities and/or interactions that are used by the tool of claim 1 to facilitate identification and extraction of nouns and verbs from textual documents, and wherein the user context is editable. Column 5, lines 46-54 of Hogue et al. describe a method of providing an interface for entering query information relating to a biomolecular interaction,

locating data corresponding to the entered query information, and displaying the data corresponding to the entered query information. It is respectfully submitted that this description is a description of a standard search, wherein a user may search the chemical graphs defining biomolecular interactions in the BIND database, and display results of the search. There is no disclosure of a user context used by a text mining tool to extract nouns and verbs from a textual document, wherein a list-based text editor lists the nouns and verbs and entities and interactions and wherein means for assigning directionality to the listed interactions facilitate disambiguating the interactions. Column 6, lines 26-32 of Hogue et al. indicate that the disclosed system may be used to study and identify biomolecular interactions. There is no disclosure or suggestion of a user context as claimed here, or of data mining textual documents to extract nouns and verbs therefrom to be used in constructing and disambiguating interactions.

With regard to claim 12, the Examiner asserted that Hogue et al. discloses direct inputting of entities and interactions into a user context. The portions of Hogue et al. referred to by the Examiner are again related to a user-constructed query for querying the BIND database. Thus, there is no disclosure of a text mining tool that uses a user context as claimed to extract nouns and verbs from a textual document.

With regard to claim 13, Column 7, lines 58-63, as noted above, disclose that the design and database samples and tools to said in web-based data entry and retrieval are described, and that a graphical system of data retrieval and data mining agents are provided that scour the data space for novel links between known interaction pathways. Again there is no mention of text mining, or of a user context as claimed. Column 20, lines 10-19, as previously noted, disclose a spider that traverses the BIND database searching for new signaling pathways. Thus, the spider traverses graphical structures, i.e., pathways, not textual documents. The new found pathways can then be experimentally evaluated. There is no disclosure here of a user context, or of editing a user context.

With regard to claim 14, column 5, lines 16-35 of Hogue et al. describe a computer system having a database with a plurality of records, each containing a reference biomolecular interaction defined by a chemical graph and descriptive information from an external database, a processor in communication with the database, and a user interface that allows a user to provide user input to the processor to selectively view information regarding a biomolecular interaction. It is respectfully submitted that this portion of Hogue et al. does not describe or suggest a user context as defined in the present specification, wherein the user context provides entities and/or interactions that are used by the tool of claim 1 to facilitate identification and extraction of nouns and verbs from textual documents, and wherein the user context is editable. Column 5, lines 46-54 of Hogue et al. describe a method of

providing an interface for entering query information relating to a biomolecular interaction, locating data corresponding to the entered query information, and displaying the data corresponding to the entered query information. It is respectfully submitted that this description is a description of a standard search, wherein a user may search the chemical graphs defining biomolecular interactions in the BIND database, and display results of the search. There is no disclosure of a user context used by a text mining tool to extract nouns and verbs from a textual document, wherein a list-based text editor lists the nouns and verbs and entities and interactions and wherein means for assigning directionality to the listed interactions facilitate disambiguating the interactions. Column 6, lines 26-32 of Hogue et al. indicate that the disclosed system may be used to study and identify biomolecular interactions. There is no disclosure or suggestion of a user context as claimed here, or of data mining textual documents to extract nouns and verbs therefrom to be used in constructing and disambiguating interactions.

With regard to claims 15, the same comments apply as above with regard to claim 14, as the Examiner relied upon the same portions of the Hogue et al. disclosure.

With regard to claim 16, column 7, lines 53-55 state that BIND draws upon NCBI data format standards, so that BIND is compatible with other public sequence and structure databases (emphasis added). This further reinforces the notion that Hogue et al. does not text mine or extract text from textual documents, as Hogue et al. is designed to be compatible with public sequence databases and structure databases. Further, since BIND is compatible with these bases, there is no conversion to a local format described. Hogue et al., column 7, lines 40-47 describe electronic management, location and/or visualization of interactions. BIND can store interaction information as a pointer to another database, a sequence, or a chemical graph. None of these possibilities refer to text or text having been converted to a local format.

With regard to claim 17, Applicants respectfully submit that Hogue et al. does not provide a means for text mining that text mines based upon contents of a user context, wherein nouns and verbs are extracted from a textual document. Column 20, lines 10-19 of Hogue et al. disclose a spider that traverses the BIND database searching for new signaling pathways. Thus, the spider traverses graphical structures, i.e., pathways, not textual documents. The new found pathways can then be experimentally evaluated. There is no disclosure here of a user context, or of editing a user context, or of local format representations of entities and interactions generated from manipulation of a biological diagram that are used to facilitate the extraction of nouns and verbs from a textual document. Nor do the portions of Hogue et al. at column 5, lines 16-35, 46-54 or column 6, lines 26-32 disclose or suggest any of these features, as noted above.

With regard to claim 18, the Examiner asserted that Hogue et al. discloses means for managing aliases at column 20, lines 37-47. Applicants respectfully disagree. Column 20, lines 37-47 describe using BIND to identify a biomolecular interaction that is similar to a reference biomolecular interactions stored in BIND. These are not aliases. Aliases occur when different names for the same entity are used. Hogue et al. refers to similar interactions, not aliases. Thus, it is respectfully submitted that claim 19 also defines over Hogue et al. for the same reasons, since Hogue et al. does not address alias management at column 20, lines 37-47.

It is respectfully submitted that claim 20 is allowable for at least the same reasons provided above with regard to claim 1, since Hogue et al. fails to disclose or suggest means for text mining to extract nouns and verbs from at least a portion of a textual document having been imported into a text viewer, or a list-based text editor that lists nouns and verbs so extracted as entities and interactions. Further, the Examiner asserted that Hogue et al. discloses a canvas area for diagrammatically representing these entities and interactions. Column 5, lines 1-5 of Hogue et al., referred to by the Examiner, refer to constructor means to create new instances from the definition of the biomolecular interactions and means to establish directional output-input links between complementary instances of the biomolecular interactions. Applicants respectfully submit that the constructor means are not described as a canvas area. Further, the biomolecular interactions referred to, are those that are already graphically stored in the BIND system, they are not generated by extracting nouns and verbs from a textual document.

It is respectfully submitted that claim 21 is allowable for at least the same reasons provided with regard to claim 20, as well as for the reasons provided above with regard to claim 2.

It is respectfully submitted that claim 22 is allowable for at least the same reasons provided with regard to claim 20, as well as for the reasons provided above with regard to claim 3.

It is respectfully submitted that claim 23 is allowable for at least the same reasons provided with regard to claim 20.

It is respectfully submitted that claim 24 is allowable for at least the same reasons provided with regard to claim 20. Further, column 4, lines 63-68 of Hogue et al. disclose visual means for making biomolecular interactions available through menus or palettes or programmatic means. The palette disclosed by Hogue et al. does not contain entities and interactions selected by a user from lists displayed by a list-based editor that lists the entities and interactions resulting from extraction of nouns and verbs from a textual document by means for text mining.

With regard to claim 25, it is respectfully submitted that claim 25 is allowable for at least the

same reasons provided with regard to claim 20. Further, it is respectfully submitted that Hogue et al. discloses neither a list-based text editor that functions as claimed, nor automatic assignment of roles based on populating a diagrammatic rendering. Column 3, lines 29-46 of Hogue et al. disclose describe a “record” of BIND, which refers to a row in a database table. Each record contains one or more fields. A record of a biomolecular interaction may contain information identifying the interaction as a chemical graph and may contain a plurality of other attributes, such as the cellular place of interaction, experimental conditions used to observe the interaction, conserved sequence comment of molecules in the interaction if they are biological sequences, information on the molecules in the interaction, description of metabolic and signaling pathways, cell cycle stages in which an interaction is involved, location of binding sites on the molecules in an interaction, chemical action mediated by the interactions, and chemical states of the molecule in the interactions. Column 7, lines 46-53 disclose that two BIND-objects that interact are held in an interaction record within BIND. BIND can also store kinetic information, bibliographic information, interaction locations, conserved sequences, mediating interaction, chemical reactions that take place and activation states of BIND-objects. It is respectfully submitted that none of the disclosure referred to by the Examiner discloses or suggests automatically assigning roles played by entities based upon populating them in a diagrammatic rendering.

It is respectfully submitted that claim 26 is allowable for at least the same reasons provided with regard to claim 20. Further, column 3, lines 6-9 of Hogue et al., which were referred to by the Examiner, disclose the ability to create and transmit images and/or text defining biomolecular interactions to a plurality of users. There is no disclosure or suggestion of freehand sketching by a user to add elements to a diagrammatic rendering on a canvas.

It is respectfully submitted that claim 27 is allowable for at least the same reasons provided with regard to claims 20 and 26.

It is respectfully submitted that claims 28 and 29 are allowable for at least the same reasons provided with regard to claims 20 and 24.

It is respectfully submitted that claim 30 is allowable for at least the same reasons provided above with regard to claim 1, since Hogue et al. fails to disclose or suggest means for text mining to extract nouns and verbs from at least a portion of a textual document having been imported into a text viewer, or a list-based text editor that lists nouns and verbs so extracted as entities and interactions. Further, the Examiner asserted that Hogue et al. discloses, at Fig. 13 and column 3, lines 1-15, means for selecting interactions and associated entities in a list-based editor, merging common entities and displaying a resulting network of the interactions. Applicants respectfully submit that they were unable

to find any disclosure of selecting interactions and associated entities in a list-based editor, or of merging common entities at column 3, lines 1-15 or in Fig. 13.

It is respectfully submitted that claim 31 is allowable for at least the same reasons provided with regard to claim 30, as well as for the reasons provided above with regard to claim 2.

It is respectfully submitted that claim 32 is allowable for at least the same reasons provided above with regard to claim 1, since Hogue et al. fails to disclose or suggest means for text mining to extract nouns and verbs from at least a portion of a textual document having been imported into a text viewer, or a list-based text editor that lists nouns and verbs so extracted as entities and interactions. Further, the Examiner asserted that Hogue et al. discloses, at column 8, lines 35-45, a diagram viewer and means for importing at least a portion of an existing biological diagram into said diagram viewer. Applicants respectfully traverse this assertion. Column 8, lines 35-45 describe a short-label field of a BIND-object and do not disclose a diagram viewer, a means for importing, or an existing biological diagram. The Examiner asserted that Hogue et al. discloses means for overlaying identified entities and interactions on at least a portion of an existing biological diagram that is displayed in a diagram viewer, and means for visually distinguishing the overlaid entities and interactions from the remainder of the diagram. The Examiner referred to column 5, lines 1-5 of Hogue et al. Column 5, lines 1-5 refer to constructor means to create new instances from the definitions of the molecular interactions and means to establish directional output-input links between complementary instances of the biomolecular interactions. There is no disclosure or suggestion of overlaying entities and interactions over an existing network and displaying such, nor of visually distinguishing the overlaid components.

It is respectfully submitted that claim 33 is allowable for at least the same reasons provided with regard to claim 32, as well as for the reasons provided above with regard to claim 2.

It is respectfully submitted that claim 34 is allowable for at least the same reasons provided with regard to claim 32.

It is respectfully submitted that claim 35 is allowable for at least the same reasons provided with regard to claim 32, as well as for the reasons provided above with regard to claims 25 and 28.

It is respectfully submitted that claim 36 is allowable for at least the same reasons provided with regard to claims 32 and 35. The Examiner asserted that Hogue et al. discloses converting at least a portion of an existing biological diagram to a local format, and based on values contained in the local format, comparing said diagrammatic renderings with corresponding parts of the existing biological diagram. The Examiner referred to column 2, lines 55-64 of Hogue et al. as support for this assertion. Column 2, lines 55-64 disclose a system for electronically managing, finding and/or visualizing

biomolecular interactions. The system, in response to data requests, can create and transmit images/and or text describing the biomolecular actions to a plurality of end users. It is respectfully submitted that this portion of Hogue et al. does not describe creating a diagrammatic rendering from nouns and verbs extracted from a textual document, converting an existing biological diagram to a local format, and comparing the diagrammatic rendering with the existing diagram, in the local format.

It is respectfully submitted that claim 37 is allowable for at least the same reasons provided with regard to claim 32.

With regard to claim 38, it is respectfully submitted that Hogue et al. fails to disclose or suggest text mining at least a portion of a textual document having been imported into a text viewer, to extract nouns and verbs therefrom, identify the nouns and verbs as biological entities, list the identified entities and interactions in a list-based text editor, or assign directionality to the listed interactions, for at least the same reasons provided above with regard to claim 1.

It is respectfully submitted that claim 39 is allowable for at least the same reasons provided with regard to claim 38 and claim 2.

It is respectfully submitted that claim 40 is allowable for at least the same reasons provided with regard to claims 38 and 8.

It is respectfully submitted that claim 41 is allowable for at least the same reasons provided with regard to claims 38 and 10.

It is respectfully submitted that claim 42 is allowable for at least the same reasons provided with regard to claims 38 and 11.

It is respectfully submitted that claim 43 is allowable for at least the same reasons provided with regard to claims 38 and 12.

It is respectfully submitted that claim 44 is allowable for at least the same reasons provided with regard to claims 38 and 16.

It is respectfully submitted that claim 45 is allowable for at least the same reasons provided with regard to claims 38 and 18.

It is respectfully submitted that claim 46 is allowable for at least the same reasons provided with regard to claims 38 and 19.

It is respectfully submitted that claim 47 is allowable for at least the same reasons provided with regard to claim 46.

It is respectfully submitted that claim 48 is allowable for at least the same reasons provided with regard to claim 38. Further, it is respectfully submitted that Hogue et al. does not disclose interactively

manipulating a biological diagram based on entities and interactions represented in said local format.

Column 2, lines 55-64 of Hogue et al. describe a system for receiving data on biomolecular interactions from a plurality of providers and processing such data to create and maintain images and/or text defining biomolecular interactions. In response to data requests, the images and/or text defining biomolecular interactions can be created and transmitted to a plurality of end-users. However, there is no disclosure or suggestion of interactively manipulating a biological diagram once it has been created.

It is respectfully submitted that claim 49 is allowable for at least the same reasons provided with regard to claims 38 and 17.

It is respectfully submitted that claim 50 is allowable for at least the same reasons provided with regard to claims 38. Further, it is respectfully submitted that Hogue et al., at column 8, lines 5-12 discloses that an interaction record contains two BIND-objects, and that these BIND-objects are themselves defined using simpler sub objects. Normally, a BIND-object that is describing a protein sequence will store a simple link to a sequence database, such as GenBank. If the sequence is not present in the public database, it can be fully represented using an NCBI-Bioseq object. Neither of these techniques refer to an entity and interaction list, wherein each entity and interaction listed points back to a location of a portion of a textual document from where the verb or noun was extracted. The first technique points to a sequence database, which contains sequences, not textual documents. The second technique is a direct representation of a sequence, and does not point back to anything.

It is respectfully submitted that claim 51 is allowable for at least the same reasons provided with regard to claims 38 and 20.

It is respectfully submitted that claim 52 is allowable for at least the same reasons provided with regard to claims 38, 51 and 25.

It is respectfully submitted that claim 53 is allowable for at least the same reasons provided with regard to claims 38, 51 and 26.

It is respectfully submitted that claim 54 is allowable for at least the same reasons provided with regard to claims 38, 51 and 28.

It is respectfully submitted that claim 55 is allowable for at least the same reasons provided with regard to claims 38, 51 and 29.

It is respectfully submitted that claim 56 is allowable for at least the same reasons provided with regard to claim 38. The Examiner asserted that Hogue et al. discloses performing a text search to identify a plurality of textual documents, importing all or a subset of the plurality of documents into the text viewer and analyzing the textual documents in batch mode to identify interactions and entities to be

listed in the list based editor. Applicants respectfully traverse these assertions. Column 5, lines 13-14 of Hogue et al. disclose a user interface that allows a user to selectively view information regarding a biomolecular interaction. Column 5 lines 26-28 disclose a user interface that allows a user to provide user input to a processor to selectively view information regarding a biomolecular interaction. Column 7, lines 19-22 state that the invention of Hogue et al is BIND and its related tools for both the management and mining of molecular interaction data. No mention of text mining is made in the referenced lines. Likewise, column 7, lines 58-63 of Hogue et al. disclose that the design and database samples and tools to aid in web-based data entry and retrieval are described, and that a graphical system of data retrieval and data mining agents are provided that scour the data space for novel links between known interaction pathways. Again there is no mention of text mining. Further, there is no disclosure or suggestion of batch processing a plurality of textual documents to extract nouns and verbs therefrom to be used to assign as entities and interactions.

It is respectfully submitted that claim 57 is allowable for at least the same reasons provided with regard to claim 38. Further, as mentioned above, it is respectfully submitted that Hogue et al. fails to disclose or suggest identifying aliases or managing the same.

It is respectfully submitted that claims 58-60 are allowable for at least the same reasons provided with regard to claim 38.

It is respectfully submitted that claim 61 is allowable for at least the same reasons provided with regard to claims 1 and 20.

It is respectfully submitted that claim 62 is allowable for at least the same reasons provided with regard to claims 61 and 27.

It is respectfully submitted that claim 63 is allowable for at least the same reasons provided with regard to claims 1 and 30.

It is respectfully submitted that claim 64 is allowable for at least the same reasons provided with regard to claims 63 and 30.

It is respectfully submitted that claim 65 is allowable for at least the same reasons provided with regard to claims 63 and 2.

It is respectfully submitted that claim 66 is allowable for at least the same reasons provided with regard to claims 65 and 36.

It is respectfully submitted that claim 67 is allowable for at least the same reasons provided with regard to claim 63. Further, it is respectfully submitted that Hogue et al., at column 20, lines 9-19, discloses using a spider to traverse BIND to search for new signaling pathways. The spider searches the

objects in BIND, traversing all pathway cross talk links looking for signaling routes that are not presently within bind. The results of this search will be potentially unknown cellular signaling pathways. This is contrary to searching and returning existing biological diagrams, as recited in claim 67.

It is respectfully submitted that claim 68 is allowable for at least the same reasons provided with regard to claim 1.

It is respectfully submitted that claim 69 is allowable for at least the same reasons provided with regard to claims 68, 2 and 50.

It is respectfully submitted that claim 70 is allowable for at least the same reasons provided with regard to claims 68 and 61.

It is respectfully submitted that claim 71 is allowable for at least the same reasons provided with regard to claims 70 and 26.

It is respectfully submitted that claim 72 is allowable for at least the same reasons provided with regard to claims 70 and 28.

It is respectfully submitted that claim 73 is allowable for at least the same reasons provided with regard to claims 70 and 29.

It is respectfully submitted that claim 74 is allowable for at least the same reasons provided with regard to claims 68 and 56.

It is respectfully submitted that claim 75 is allowable for at least the same reasons provided with regard to claim 68 and because Hogue et al. does not disclose or suggest identifying aliases or performing operations on aliases.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1-75 under 35 U.S.C. Section 102(e) as being anticipated by Hogue et al., U.S. Patent No. 6,745,204, as being inappropriate.

Conclusion

Applicants submit that all of the claims are in condition for allowance, which action is requested. If the Examiner finds that a telephone conference would expedite the prosecution of this application, please telephone the undersigned at the number provided.

The Commissioner is hereby authorized to charge any underpayment of fees associated with this communication, including any necessary fees for extensions of time, or credit any overpayment to Deposit Account No. 50-1078, order number 10030986-1.

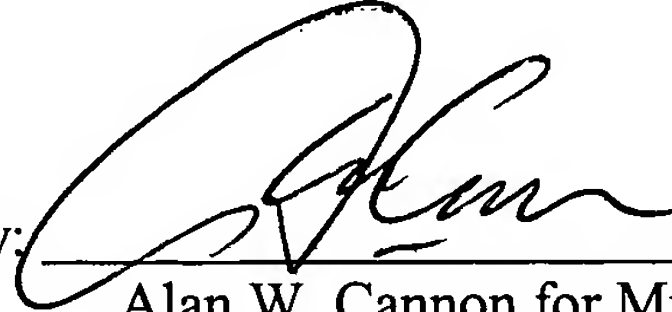
Respectfully submitted,

LAW OFFICE OF ALAN W. CANNON

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6/29/06

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